



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101828531
Source: EFW0
Date Processed by STIC: 8/13/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 101828531

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/828,531

DATE: 08/13/2004

TIME: 16:08:29

Input Set : A:\NASA00301.ST25.txt

Output Set: N:\CRF4\08132004\J828531.raw

3 <110> APPLICANT: Atassi, M. Z.
 4 Morrision, D. R.
 6 <120> TITLE OF INVENTION: Molecular-specific Urokinase Antibodies
 8 <130> FILE REFERENCE: MSC-21947-1-CU
 10 <140> CURRENT APPLICATION NUMBER: 10/828,531
 11 <141> CURRENT FILING DATE: 2004-04-14
 13 <160> NUMBER OF SEQ ID NOS: 17
 15 <170> SOFTWARE: PatentIn version 3.1

17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 15
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Peptide
 22 <400> SEQUENCE: 1
 24 Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
 25 1 5 10 15

Does Not Comply
 Corrected Diskette Needed
 (PJ-TS) ←

28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 15
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Peptide
 33 <400> SEQUENCE: 2
 35 Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
 36 1 5 10 15

← Mandatory
 <213> response
 has to be
 either artificial
unknown or
Genus/
Species.

39 <210> SEQ ID NO: 3
 40 <211> LENGTH: 10
 41 <212> TYPE: PRT
 42 <213> ORGANISM: Peptide
 44 <400> SEQUENCE: 3
 46 Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro
 47 1 5 10

50 <210> SEQ ID NO: 4
 51 <211> LENGTH: 11
 52 <212> TYPE: PRT
 53 <213> ORGANISM: Peptide
 55 <400> SEQUENCE: 4
 57 Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp Cys
 58 1 5 10

61 <210> SEQ ID NO: 5
 62 <211> LENGTH: 10
 63 <212> TYPE: PRT
 64 <213> ORGANISM: Peptide
 66 <400> SEQUENCE: 5
 68 Cys Met Val His Asp Gly Ala Asp Gly Lys
 69 1 5 10

↑ please see item # 10 for all
errors above, on error
 summary sheet. 8/13/04

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Input Set : A:\NASA00301.ST25.txt

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72 <210> SEQ ID NO: 6
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 74 <212> TYPE: PRT
 75 <213> ORGANISM: Peptide
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 80 1 5
 83 <210> SEQ ID NO: 7
 84 <211> LENGTH: 13
 85 <212> TYPE: PRT
 86 <213> ORGANISM: Peptide
 88 <400> SEQUENCE: 7
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 91 1 5 10
 94 <210> SEQ ID NO: 8
 95 <211> LENGTH: 11
 96 <212> TYPE: PRT
 97 <213> ORGANISM: Peptide
 99 <400> SEQUENCE: 8
 101 Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr
 102 1 5 10
 105 <210> SEQ ID NO: 9
 106 <211> LENGTH: 12
 107 <212> TYPE: PRT
 108 <213> ORGANISM: Peptide
 110 <220> FEATURE:
 111 <221> NAME/KEY: Misc_Feature
 112 <222> LOCATION: (4)..(6)
 113 <223> OTHER INFORMATION: n = Anything
 116 <400> SEQUENCE: 9
 118 Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys
 119 1 5 10
 122 <210> SEQ ID NO: 10
 123 <211> LENGTH: 12
 124 <212> TYPE: PRT
 125 <213> ORGANISM: Peptide
 127 <220> FEATURE:
 128 <221> NAME/KEY: Misc_Feature
 129 <222> LOCATION: (4)..(4)
 130 <223> OTHER INFORMATION: n = anything
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 135 Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys
 136 1 5 10
 139 <210> SEQ ID NO: 11
 140 <211> LENGTH: 24
 141 <212> TYPE: PRT
 142 <213> ORGANISM: Peptide
 144 <400> SEQUENCE: 11
 146 Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu

"N"s CAN NOT
 be represented
 in Amino Acid
sequences.

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Input Set : A:\NASA00301.ST25.txt

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✓ SAME
errors

```

147 1          5          10          15
150 Val Thr Thr Thr Lys Met Leu Cys
151          20
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155 <211> LENGTH: 11
156 <212> TYPE: PRT
157 <213> ORGANISM: Peptide
159 <220> FEATURE:
160 <221> NAME/KEY: Misc_feature
161 <222> LOCATION: (7)..(7)
162 <223> OTHER INFORMATION: n = anything
165 <400> SEQUENCE: 12
167 Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
168 1          5          10
171 <210> SEQ ID NO: 13
172 <211> LENGTH: 7
173 <212> TYPE: PRT
174 <213> ORGANISM: Peptide
176 <400> SEQUENCE: 13
178 Pro Arg Phe Lys Ile Ile Gly
179 1          5
182 <210> SEQ ID NO: 14
183 <211> LENGTH: 10
184 <212> TYPE: PRT
185 <213> ORGANISM: Peptide
187 <400> SEQUENCE: 14
189 Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu
190 1          5          10
193 <210> SEQ ID NO: 15
194 <211> LENGTH: 10
195 <212> TYPE: PRT
196 <213> ORGANISM: Peptide
198 <400> SEQUENCE: 15
200 Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly
201 1          5          10
204 <210> SEQ ID NO: 16
205 <211> LENGTH: 411
206 <212> TYPE: PRT
207 <213> ORGANISM: Peptide
209 <220> FEATURE:
210 <221> NAME/KEY: Misc_feature
211 <222> LOCATION: (2)..(407)
212 <223> OTHER INFORMATION: n = anything
215 <400> SEQUENCE: 16
217 Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
218 1          5          10          15
221 Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
222          20          25          30
225 Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys

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Input Set : A:\NASA00301.ST25.txt

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226          35          40          45
229 Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
230      50          55          60
233 Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
234 65          70          75          80
237 Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
238          85          90          95
241 Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
242          100          105          110
245 Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
246          115          120          125
249 His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
250          130          135          140
253 Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
254 145          150          155          160
257 Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
258          165          170          175
261 Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
262          180          185          190
265 Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
266          195          200          205
269 Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
270          210          215          220
273 Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
274 225          230          235          240
277 Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
278          245          250          255
281 Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
282          260          265          270
285 Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
286          275          280          285
289 Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290          290          295          300
293 Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
294 305          310          315          320
297 Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
298          325          330          335
301 Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
302          340          345          350
305 Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
306          355          360          365
309 Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
310          370          375          380
313 Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
314 385          390          395          400
317 Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
318          405          410
321 <210> SEQ ID NO: 17
322 <211> LENGTH: 9

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TIME: 16:08:29

Input Set : A:\NASA00301.ST25.txt

Output Set: N:\CRF4\08132004\J828531.raw

323 <212> TYPE: PRT

324 <213> ORGANISM: Peptide

326 <400> SEQUENCE: 17

328 Ala Asp Asp Gly Lys Lys Pro Ser Ser

329 1 5

- Same error

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/828,531**

DATE: 08/13/2004

TIME: 16:08:30

Input Set : **A:\NASA00301.ST25.txt**

Output Set: **N:\CRF4\08132004\J828531.raw**